



# Metagenomic Sequencing Unravels Gene Fragments with Phylogenetic Signatures of O<sub>2</sub>-Tolerant NiFe Membrane-Bound Hydrogenases in Lacustrine Sediment

Jillian M. Couto<sup>1</sup> · Umer Zeeshan Ijaz<sup>1</sup> · Vernon R. Phoenix<sup>2</sup> · Melanie Schirmer<sup>1</sup> · William T. Sloan<sup>1</sup>

Received: 10 February 2015 / Accepted: 19 April 2015 / Published online: 5 June 2015  
© The Author(s) 2015. This article is published with open access at Springerlink.com

**Abstract** Many promising hydrogen technologies utilising hydrogenase enzymes have been slowed by the fact that most hydrogenases are extremely sensitive to O<sub>2</sub>. Within the group 1 membrane-bound NiFe hydrogenase, naturally occurring tolerant enzymes do exist, and O<sub>2</sub> tolerance has been largely attributed to changes in iron–sulphur clusters coordinated by different numbers of cysteine residues in the enzyme’s small subunit. Indeed, previous work has provided a robust phylogenetic signature of O<sub>2</sub> tolerance [1], which when combined with new sequencing technologies makes bio prospecting in nature a far more viable endeavour. However, making sense of such a vast diversity is still challenging and could be simplified if known species with O<sub>2</sub>-tolerant enzymes were annotated with information on metabolism and natural environments. Here, we utilised a bioinformatics approach to compare O<sub>2</sub>-tolerant and sensitive membrane-bound NiFe hydrogenases from 177 bacterial species with fully sequenced genomes for differences in their taxonomy, O<sub>2</sub> requirements, and natural environment. Following this, we interrogated a metagenome from lacustrine surface sediment for novel hydrogenases via high-throughput shotgun DNA sequencing using the Illumina<sup>TM</sup> MiSeq platform. We found 44 new NiFe

group 1 membrane-bound hydrogenase sequence fragments, five of which segregated with the tolerant group on the phylogenetic tree of the enzyme’s small subunit, and four with the large subunit, indicating de novo O<sub>2</sub>-tolerant protein sequences that could help engineer more efficient hydrogenases.

## Introduction

The microbial world is a rich reserve of species and metabolic capabilities, which are being exploited to tackle grand challenges in energy, biotechnology and drug discovery. However, despite our knowledge of this vast diversity, we appear to rely on a few well-characterised organisms in biotechnological applications. Thus, there is a tendency when optimizing a biotechnology process to genetically engineer these organisms rather than seek out more efficient natural organisms. While genetic engineering can be used to enhance performance, it does not always lead to a superior enzyme as has been the case with O<sub>2</sub> tolerance and NiFe hydrogenases [2].

Hydrogenases are enzymes of great biotechnological interest because they catalyse the H<sub>2</sub> half-cell reaction [2H<sup>+</sup> + 2e<sup>−</sup> ⇌ H<sub>2</sub>] that can be manipulated to produce hydrogen from sunlight [3, 4] or sustainably use hydrogen in fuel cells driven by biocatalysts [5, 6]. However, while all three types of hydrogenases, [Ni–Fe], [Fe–Fe] and [Fe-only], can catalyse this reaction for the vast majority of enzymes that we know about, this reaction is severely attenuated, or even irreversibly halted, in the presence of O<sub>2</sub>. Given that O<sub>2</sub> is either present or produced in every major reaction exploited by these proposed technologies, this intolerance is a major stumbling block that must be

**Electronic supplementary material** The online version of this article (doi:10.1007/s00284-015-0846-2) contains supplementary material, which is available to authorized users.

✉ Jillian M. Couto  
Jillian.Couto@glasgow.ac.uk

<sup>1</sup> Division of Infrastructure and Environment, School of Engineering, University of Glasgow, Rankine Building, Level 5, Glasgow G12 8LT, Scotland, UK

<sup>2</sup> School of Geographical and Earth Science, University of Glasgow, Glasgow G12 8QQ, Scotland, UK

overcome [4, 5]. Of all the different types of hydrogenases, the membrane-bound NiFe subtype (MBH) has a few well-characterised O<sub>2</sub>-tolerant members. One in particular, from the bacteria *Ralstonia eutropha*, is currently utilised in experimental enzymatic fuel cells (EFCs) [5]. However, this aero tolerance comes with the cost of both a total bias towards H<sub>2</sub> oxidation [7–10] and a decreased efficiency [11] when compared with O<sub>2</sub> sensitive hydrogenases (herein referred to as standard hydrogenases) [12]. As the ideal hydrogenase for many of these technologies would be both oxygen tolerant and efficient, significant work has gone into creating such an enzyme via genetic manipulation [7, 8, 13, 14]. Although efforts thus far have met with little success [2], when combined with research on the structural chemistry [15–21] of MBHs, these studies have delivered significant insight into the mechanisms and gene sequence that are responsible for O<sub>2</sub> tolerance.

Tolerance has been linked to specific amino acid residues mostly in the small subunit ( $\alpha$ ) and to a lesser extent in the large subunit ( $\beta$ ) of the NiFe MBH. The bulk of the evidence shows that O<sub>2</sub> tolerance is a function of the proximal Fe–S cluster coordinated by key cysteine residues in the enzyme's small subunit [1, 8, 14]. Specifically, O<sub>2</sub>-tolerant enzymes possess six cysteine residues (6C group) instead of the typical four conserved cysteine residues (4C group) found in standard hydrogenases. There is also emerging evidence from the enzyme's large subunit that shows a histidine (H229) residue could serve to further stabilise the proximal cluster in the presence of O<sub>2</sub> [22, 23]. Taken together, this information produces a reliable phylogenetic signature that can be used to identify potential de novo O<sub>2</sub>-tolerant enzymes from sequence alone.

Indeed, a recent study identified at least 30 additional MBH sequences with the phylogenetic signature suggestive of O<sub>2</sub> tolerance from publically available fully sequenced genomes of microbes that can be cultured [1]. Cultured isolates represent a small fraction (<1 %) of the diversity of bacteria on the earth [24], so with the vagaries of evolution acting over billions of years on MBH in distantly related organisms it seems reasonable to speculate that there may be an untapped diversity of O<sub>2</sub>-tolerant enzymes in nature. However, sequence information will be of little use if not provided within the context of the organisms' natural habitat as these organisms have evolved to exploit these diverse environments by fine-tuning their metabolisms to these conditions. Therefore, differences in natural habitats and subtleties of O<sub>2</sub> metabolisms of an organism could have shaped an enzyme that is more biotechnologically suitable than the ones currently under use.

In this study, we interrogated publically available MBH sequences that had the phylogenetic signature of O<sub>2</sub> tolerance for differences in taxonomic group, natural

environments and oxygen requirements. Following this, we used whole metagenome next generation sequencing to isolate novel O<sub>2</sub>-tolerant NiFe MBH sequence fragments from an environmental sample.

## Methods

### Additions Details can be Found in the Supplementary Text

#### Database Mining: NCBI PSI-Blast Search

NiFe membrane-bound hydrogenase sequences were extracted from the National Centre for Biotechnology Information ([www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov)) database that contained 1087 completed microbial genomes at time of query. Searches were conducted with PSI-BLAST [25]. The default setting was changed to return 500 hits. Any query with less than 80 % coverage was eliminated.

#### Environmental Descriptors in SEQenv

The SEQenv pipeline (<https://bitbucket.org/seqenv/seqenv/src>) retrieves hits to highly similar reference sequences from NCBI and uses a text-mining module to identify a structured and controlled vocabulary of environmental descriptive terms, Environmental Ontology (EnvO) (<http://environmentontology.org>), mentioned in both associated PubMed abstracts and the “Isolation Source” field entry for the reference hits. We have used version 0.8 of SEQenv that contained a filtered list of approximately 1200 EnvO terms organized into three main branches, namely environmental material, environmental feature and biome. Thus, for each of the 177-hydrogenase sequences, we obtained the EnvO terms along with their frequency of occurrences.

#### Phylogenetic Trees

Trees were constructed with MrBayes v 3.2 [26] using a model that integrated over a set of fixed amino acid matrices (aamodelpr = mixed) [27] with no heated chains. The number of cycles for the MCMC algorithm was set to 2,500,000 generations, with trees sampled every 500 generations using an MCMC analysis.

#### Environmental Samples and Metagenomic Sequencing

Our main field site was in the Lake Torneträsk region (68°21'N, 19°02'E) in Abisko, Sweden. Sampling was conducted from a rowboat using an Eckmann Grab sampler, which collects the top 10–15 cm of sediment. Sediment samples (water depth = 4 m; temp. = 11.5 °C; pH

7.02 surface water temp. = 14.3 °C; air = 17 °C) were immediately sealed in sterile containers and imported back to the United Kingdom (UK) via a permit granted by the UK Plant Health Service and Science and Advice for Scottish Agriculture (SASA). Metagenomic DNA was extracted using the FastDNA<sup>TM</sup> SPIN kit for soil (MP biomedical; Santa Ana, CA, USA). Shotgun libraries were constructed and sequenced (paired-end reads) at the Centre for Genomic Research at the University of Liverpool using the Illumina<sup>®</sup> MiSeq platform. Sequences utilised in this study are provided as supplementary material.

Paired-end reads were filtered and quality trimmed in 'Sickle' [28] with the sliding window approach to trim regions when the average base quality dropped below 20. A 10-bp length threshold was used to discard reads that fall below this length after trimming. IDBA-UD [29], an iterative De Bruijn Graph de novo assembler, was used to assemble contigs by iterating from Kmer size of 21–121 and using a pre-correction of reads before assembly. We obtained assembled contigs with a N50 score of 521 with the length of the largest contig being 104,564 bp. The obtained contigs were then run through 'Prokka' [30] to obtain annotated Genbank files containing coding sequence regions (CDS) for each contig.

## Results

Database mining identified 177 sequences for the large and small subunit of the NiFe MBH. We focused on the small subunit, as the evidence for its role in O<sub>2</sub> tolerance is extremely compelling [1, 8, 14]. Following a sequence alignment to analyse the phylogenetic signature of each enzyme (Table S1), they were classed as O<sub>2</sub> tolerant if they possessed conserved cysteines (6C;  $n = 63$ ) at six key amino acid positions in the small subunit or standard (4C;  $n = 114$ ) if they had glycine substituted for cysteine at two of these six positions. We then compared the taxonomic group, natural environments and oxygen requirements of these microbes to test for differences. We found an unequal distribution of 4C and 6C enzymes for all three measures (Fig. 1). The taxonomic groups were unequally distributed amongst the 4C and 6C enzymes (Fig. 1a). Notably, the (CFB) group and Green sulphur bacteria (GSB) only contained 6C enzymes, while the Euryarchaeota, Green non-sulphur bacteria (GNS) and  $\epsilon$ -proteobacteria only contained 4C enzymes. Similarly,  $\delta$ -proteobacteria were disproportionately (8.02-fold difference) higher in the 4C group, while the  $\alpha$ - (17.77-fold) and  $\beta$ - proteobacteria (16.84-fold) were over-represented in the 6C group.

Natural environments returned from SEQenv were also unequally distributed amongst the two groups of enzymes (Fig. 1b). Overall, the 4C group contained organisms that

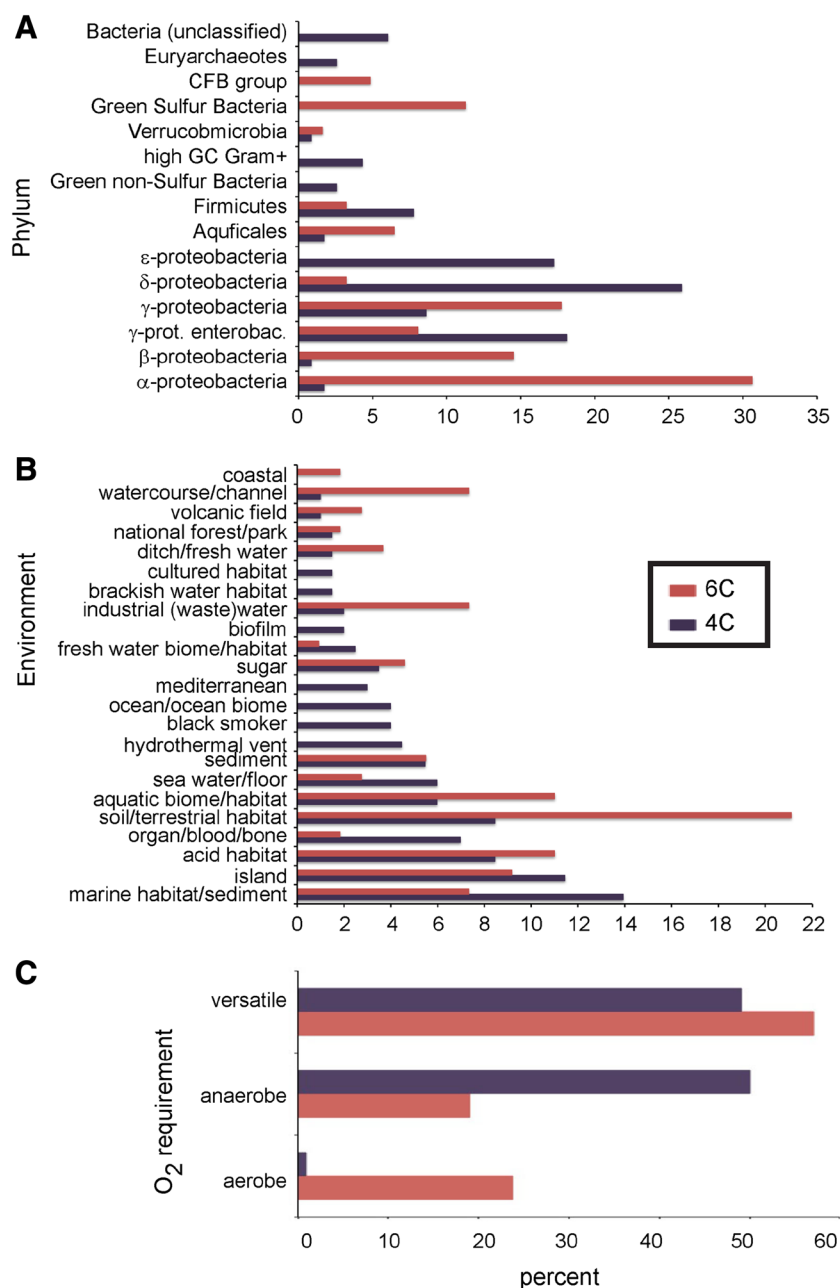
inhabited more saline, marine environments and environments of geothermal significance, while organisms with 6C enzymes appeared to be more prevalent in terrestrial and freshwater environments.

Microbes were classed as aerobes, anaerobes or versatile in order to assess their O<sub>2</sub> requirements. The versatile organisms appeared in roughly equal proportions in both the 4C and 6C groups, while there was a striking difference between the distribution of aerobes and anaerobes (Fig. 1c). The 6C group contained 28.5-fold more aerobes than the 4C group. Conversely, there were 2.54-fold more anaerobes in the 4C group compared with the 6C group.

Aquatic ecosystems are important for the flux of H<sub>2</sub> in and out of the environment and have been investigated previously for new hydrogenases [31, 32]. To explore this diversity further, we extracted metagenomic DNA from sediment from a subarctic lake in North Sweden (68°21'N, 19°02'E) and directly sequenced the metagenome using the Illumina<sup>TM</sup> MiSeq platform. Following contig assembly, 241 sequences could be annotated with the enzyme commission (E.C.) number 1.12. -. -, identifying them as hydrogenases. Of these, 18 sequences could be identified as group 1 MBH small subunits, and 26 sequences could be identified as the large subunit of the group 1 MBH. These sequences ranged in length from full proteins to 35 amino acid fragments. All 44 sequences were compared against the NCBI non-redundant protein sequence database using PSI-BLAST [25]. Of the small subunit sequences, one 362 amino acid query (sequence 20) was an exact match to a known sequence representing multiple species from the *Rhodocyclaceae* (GI: 518758527) family (Table S2). For the large subunit, a 38 amino acid fragment was an exact match to *Asticcacaulis* sp. AC466 (GI: 557832447). The rest were partial matches, suggesting that they could be sequences from previously uncharacterised organisms (Table S2).

Utilising the 177 database sequences and a Bayesian inference, we estimated the phylogeny of both the small and large subunit with a Markov Chain Monte Carlo (MCMC) approximation to construct trees (Figures S1–S5) onto which we could place the 44 sequence fragments from our metagenomic analysis. For the small subunit, all 18 sequences appeared on different branches with distinct lengths (Fig. 2, 6C; Figure S4, 4C). Of these, sequences 133, 229, 218, 230 and 20 segregated within the 6C group (Fig. 2). Sequence 20 in particular is a full-length protein and has the critical cysteine residues,  $\alpha_{62}$  and  $\alpha_{163}$ . Sequence 218 is a partial fragment that also contains a cysteine residue at  $\alpha_{163}$ . The Fe–S cluster co-ordinating region was not recovered for the rest of the sequences; however, both sequence 229 and 230 segregate with the 6C enzymes suggesting that they too are O<sub>2</sub> tolerant. Fragment 133 was only 55 residues in length and grouped with both

**Fig. 1** Comparative analysis of Phylum, natural environment and oxygen requirements of 4C and 6C membrane-bound hydrogenases. The distribution of Phyla (a), natural environment (b) and oxygen requirements (c) within the 4C and 6C groups was compared. Bars representing the 6C enzymes are shown in red, while 4C enzymes are shown in dark purple. The horizontal axes show percent per group



the 6C CFB organisms and the 4C *G. thermoglucosidasius*, suggesting that it could be from either group.

Similarly, the 26 large subunit sequences appeared to be distinct species, with fragment numbers 6, 39, 232 and 181 segregating with the 6C enzymes (Figure S5). Of these, sequence 232 is nearly full-length and segregates with *R. gelatinosus* and *C. metallidurans*, two well-characterised O<sub>2</sub>-tolerant hydrogenases, suggesting that it too is an O<sub>2</sub>-tolerant hydrogenase from the *β-proteobacteria* phylum. The rest were short fragments but grouped with 6C containing hydrogenases.

## Discussion

The immediate need for efficient biotechnologies to solve current problems such as sustainable sources of energy has driven us to explore the microbial landscape for unique organisms and enzymes. However on its own, sequence information is not enough and needs to be paired with contextual information about the organism and the environment it inhabits. The observation that the 4C and 6C enzymes are not randomly distributed across phyla, natural environments or oxygen requirements suggests that these

**Fig. 2** Phylogenetic tree of sequences for the enzyme's small subunit with segregating 6C environmental metagenomic fragments. The fragments 133, 229, 218, 230 and 20 segregate within the 6C group. The 4C group (grey triangle) has been collapsed but can be viewed in detail in Figure S4. Fragment 166 appears to form a distinct group. The scale refers to 0.3 expected changes per site. An asterisk marks the four standard hydrogenase (SH)/4C hydrogenases from the *Firmicutes* phylum that cluster within the 6C group. Unless otherwise indicated, all enzymes are 6C



factors have influenced the evolution of these enzymes. Overall, there appears to be a shift from harsh, nutrient poor environments, to more anodyne, nutrient-rich environment. The 4C enzyme grouping mostly contained organisms that could metabolise sulphur and metals anaerobically. The 6C enzyme group contained organisms with aerobic metabolisms as well as many species that could either photosynthesize or metabolise nitrogen. This supports the idea of a redox up-shift via high-potential terminal electron acceptors within the 6C group [1]. An exception is the enzyme from *R. eutropha*, utilised in some experimental biotechnologies [3–5]. This organism exploits the relatively redox poor “Knallgas” reaction despite being part of the 6C group. A more superior

enzyme could be purified from phylogenetically related organisms that exploit high-potential redox reactions. In particular, the purple non-sulphur bacteria display an array of metabolic capabilities and are actively being investigated for their potential in  $H_2$  technologies [33–40]. Having evolved different modifications, some of which may provide increased efficiency, exploring these groups might greatly benefit the engineered systems.

The presence of  $O_2$  in the organism's natural environment could also affect enzyme efficiency. In environments with a flux of  $O_2$ , there is still the possibility that when  $O_2$  is present, the MBH is either not expressed or is expressed but has a lowered efficiency. A relationship between expression, aerobicity and enzyme function was demonstrated with hyd-



5 in *S. enterica* [22, 41]. Twenty-four percent of the enzymes from our study were detected in predominantly aerobic environments with a potentially constant exposure to O<sub>2</sub>. Therefore, one could speculate that aerobes would possess hydrogenases that are extremely tolerant and potentially more efficient than the ones in the versatile group and the obligate anaerobes. Indeed, in experiments, the aerobe *H. marinus* retained a higher percentage of activity compared to the microaerophilic *R. eutropha* after exposure to air [42]. The aerobes *B. vietnamiensis* G4, *P. naphthalenivorans* CJ2 and *M. petroleiphilum* PM1 have phylogenetically related hydrogenases to *R. eutropha* (Figure S1) that might have evolved greater efficiency due to their aerobic heterotrophic lifestyles.

The current study recovered MBH sequence fragments via shotgun high-throughput sequencing of metagenomic DNA from an environmental sample. Although the number of MBH sequence fragments recovered in our study was lower than expected, it is comparable to work utilising similar techniques to discover novel hydrogenases from the global ocean survey of surface waters [32]. Of the five new 6C sequences, four segregate with aerobic/facultative heterotrophic  $\alpha$ - and  $\beta$ -proteobacteria on the small subunit tree, and similar to their cultured neighbours, could also make use of high-potential redox couples. The full-length small subunit sequence 20 from the *Rhodocyclales* family (Table S2) segregates with the aerobic  $\beta$ -proteobacteria *Methylibium petroleiphilum* and *Polaromonas naphthalenivorans*. Both are aquatic aerobic heterotrophs that can use methyl tert-butyl ether [43] and Naphthalene [44], respectively, as sole carbon sources. Similarly, the close-to-full-length fragment 218 segregates with *Decloromonas aromatica* species and is most likely from this or a closely related organism.

The phylogenetic tree and analyses of taxonomic groups, natural environments and oxygen requirements enabled us to place all 44 de novo MBH sequence fragment amongst the 177 MBH identified from the database search providing a powerful tool for bio-inspired enzyme engineering. Using the database analysis, we can now make use of well-characterised biology and couple it to the uniqueness offered by an untapped reserve of natural diversity, greatly enhancing a simple BLAST search. It stands to reason that these de novo sequences contain novel combinations of amino acid residues that could be utilised to engineer the hydrogenases from organisms that lend themselves well to pure-culture. In addition, identifying related sequences can target primer design and identify genomes of organisms that can serve as a scaffold for downstream procedures to assemble and retrieve 'missing' gene information in order to re-create a full enzyme.

**Acknowledgments** This work has been funded by an EPSRC Supergen biofuels (EP/H019480/1) and an EPSRC Frontiers in

Engineering (EP/K038885/1) Grant held by WTS. The Field expedition was funded by a John Robertson Bequest grant from the University of Glasgow to JMC and a grant from the Carnegie Trust for the Universities of Scotland to VRP. UZI is funded by a NERC independent research fellowship, NE/L011956/1. We are grateful for the advice from scientists at the Abisko Scientific Research Station in Sweden. The authors declare no competing or conflicts of interest.

**Open Access** This article is distributed under the terms of the Creative Commons Attribution 4.0 International License (<http://creativecommons.org/licenses/by/4.0/>), which permits unrestricted use, distribution, and reproduction in any medium, provided you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons license, and indicate if changes were made.

## References

1. Pandelia ME, Lubitz W (1817) Nitschke W (2012) Evolution and diversification of Group 1 [NiFe] hydrogenases. Is there a phylogenetic marker for O(2)-tolerance? *Biochim Biophys Acta* 9:1565–1575. doi:[10.1016/j.bbabbio.2012.04.012](https://doi.org/10.1016/j.bbabbio.2012.04.012)
2. Leroux F, Liebgott P-P, Cournac L, Richaud P, Kpebe A, Burlat B, Guigliarelli B, Bertrand P, Leger C, Rousset M, Dementin S (2010) Is engineering O(2)-tolerant hydrogenases just a matter of reproducing the active sites of the naturally occurring O(2)-resistant enzymes? *Int J Hydrogen Energy* 35(19):10770–10777. doi:[10.1016/j.ijhydene.2010.02.071](https://doi.org/10.1016/j.ijhydene.2010.02.071)
3. Reisner E (2011) Solar Hydrogen Evolution with Hydrogenases: from Natural to Hybrid Systems. *Eur J Inorg Chem* 7:1005–1016. doi:[10.1002/ejic.201000986](https://doi.org/10.1002/ejic.201000986)
4. Friedrich B, Fritsch J, Lenz O (2011) Oxygen-tolerant hydrogenases in hydrogen-based technologies. *Curr Opin Biotechnol* 22(3):358–364. doi:[10.1016/j.copbio.2011.01.006](https://doi.org/10.1016/j.copbio.2011.01.006)
5. Cracknell JA, Vincent KA, Armstrong FA (2008) Enzymes as working or inspirational electrocatalysts for fuel cells and electrolysis. *Chem Rev* 108(7):2439–2461. doi:[10.1021/cr0680639](https://doi.org/10.1021/cr0680639)
6. Woolerton TW, Sheard S, Chaudhary YS, Armstrong FA (2012) Enzyme and bio-inspired electrocatalysts in solar fuel devices. *Energy Environ Sci* 5:7470–7490
7. Liebgott P-P, de Lacey AL, Burlat B, Cournac L, Richaud P, Brugna M, Fernandez VM, Guigliarelli B, Rousset M, Leger C, Dementin S (2011) Original Design of an Oxygen-Tolerant NiFe Hydrogenase: major effect of a Valine-to-Cysteine Mutation near the Active Site. *J Am Chem Soc* 133(4):986–997. doi:[10.1021/ja108787s](https://doi.org/10.1021/ja108787s)
8. Lukey MJ, Roessler MM, Parkin A, Evans RM, Davies RA, Lenz O, Friedrich B, Sargent F, Armstrong FA (2011) Oxygen-Tolerant NiFe -Hydrogenases: the individual and collective importance of supernumerary cysteines at the proximal Fe-S cluster. *J Am Chem Soc* 133(42):16881–16892. doi:[10.1021/ja205393w](https://doi.org/10.1021/ja205393w)
9. Lukey MJ, Parkin A, Roessler MM, Murphy BJ, Harmer J, Palmer T, Sargent F, Armstrong FA (2010) How *Escherichia coli* is equipped to oxidize hydrogen under different redox conditions. *J Biol Chem* 285(6):3928–3938. doi:[10.1074/jbc.M109.067751](https://doi.org/10.1074/jbc.M109.067751)
10. Abou Hamdan A, Dementin S, Liebgott PP, Gutierrez-Sanz O, Richaud P, De Lacey AL, Rousset M, Bertrand P, Cournac L, Leger C (2012) Understanding and tuning the catalytic bias of hydrogenase. *J Am Chem Soc* 134(20):8368–8371. doi:[10.1021/ja301802r](https://doi.org/10.1021/ja301802r)
11. Shafaat HS, Rudiger O, Ogata H (1827) Lubitz W (2013) [NiFe] hydrogenases: a common active site for hydrogen metabolism under diverse conditions. *Biochim Biophys Acta* 8–9:986–1002. doi:[10.1016/j.bbabbio.2013.01.015](https://doi.org/10.1016/j.bbabbio.2013.01.015)

12. Vincent KA, Cracknell JA, Parkin A, Armstrong FA (2005) Hydrogen cycling by enzymes: electrocatalysis and implications for future energy technology. *Dalton Trans* 21:3397–3403. doi:[10.1039/b508520a](https://doi.org/10.1039/b508520a)
13. Ludwig M, Cracknell JA, Vincent KA, Armstrong FA, Lenz O (2009) Oxygen-tolerant H<sub>2</sub> oxidation by membrane-bound [NiFe] hydrogenases of *Ralstonia* species. coping with low level H<sub>2</sub> in air. *J Biol Chem* 284(1):465–477. doi:[10.1074/jbc.M803676200](https://doi.org/10.1074/jbc.M803676200)
14. Goris T, Wait AF, Saggu M, Fritsch J, Heidary N, Stein M, Zebger I, Lendzian F, Armstrong FA, Friedrich B, Lenz O (2011) A unique iron-sulfur cluster is crucial for oxygen tolerance of a [NiFe]-hydrogenase. *Nat Chem Biol* 7(5):310–318. doi:[10.1038/nchembio.555](https://doi.org/10.1038/nchembio.555)
15. Shomura Y, Yoon K-S, Nishihara H, Higuchi Y (2011) Structural basis for a 4Fe-3S cluster in the oxygen-tolerant membrane-bound NiFe -hydrogenase. *Nature* 479(7372):253–256. doi:[10.1038/nature10504](https://doi.org/10.1038/nature10504)
16. Horch M, Schoknecht J, Mroginski MA, Lenz O, Hildebrandt P, Zebger I (2014) Resonance raman spectroscopy on [NiFe] Hydrogenase provides structural insights into catalytic intermediates and reactions. *J Am Chem Soc.* doi:[10.1021/ja505119q](https://doi.org/10.1021/ja505119q)
17. Fritsch J, Scheerer P, Frielingsdorf S, Kroschinsky S, Friedrich B, Lenz O, Spahn CMT (2011) The crystal structure of an oxygen-tolerant hydrogenase uncovers a novel iron-sulphur centre. *Nature* 479(7372):249–252. doi:[10.1038/nature10505](https://doi.org/10.1038/nature10505)
18. Fritsch J, Lenz O, Friedrich B (2013) Structure, function and biosynthesis of O<sub>2</sub>-tolerant hydrogenases. *Nat Rev Microbiol* 11(2):106–114. doi:[10.1038/nrmicro2940](https://doi.org/10.1038/nrmicro2940)
19. Volbeda A, Amara P, Darnault C, Mouesca JM, Parkin A, Roessler MM, Armstrong FA, Fontecilla-Camps JC (2012) X-ray crystallographic and computational studies of the O<sub>2</sub>-tolerant [NiFe]-hydrogenase 1 from *Escherichia coli*. *Proc Natl Acad Sci USA* 109(14):5305–5310. doi:[10.1073/pnas.1119806109](https://doi.org/10.1073/pnas.1119806109)
20. Pandelia ME, Nitschke W, Infossi P, Giudici-Orticoni MT, Bill E, Lubitz W (2011) Characterization of a unique [FeS] cluster in the electron transfer chain of the oxygen tolerant [NiFe] hydrogenase from *Aquifex aeolicus*. *Proc Natl Acad Sci USA* 108(15):6097–6102. doi:[10.1073/pnas.1100610108](https://doi.org/10.1073/pnas.1100610108)
21. Volbeda A, Charon MH, Piras C, Hatchikian EC, Frey M, Fontecilla-Camps JC (1995) Crystal structure of the nickel-iron hydrogenase from *Desulfovibrio gigas*. *Nature* 373(6515):580–587. doi:[10.1038/373580a0](https://doi.org/10.1038/373580a0)
22. Bowman L, Flanagan L, Fyfe PK, Parkin A, Hunter WN, Sargent F (2014) How the structure of the large subunit controls function in an oxygen-tolerant [NiFe]-hydrogenase. *Biochem J* 458(3):449–458. doi:[10.1042/bj20131520](https://doi.org/10.1042/bj20131520)
23. Frielingsdorf S, Fritsch J, Schmidt A, Hammer M, Lowenstein J, Siebert E, Pelmschikov V, Jaenicke T, Kalms J, Rippers Y, Lendzian F, Zebger I, Teutloff C, Kaupp M, Bittl R, Hildebrandt P, Friedrich B, Lenz O, Scheerer P (2014) Reversible [4Fe-3S] cluster morphing in an O<sub>2</sub>-tolerant [NiFe] hydrogenase. *Nat Chem Biol* 10(5):378–385. doi:[10.1038/nchembio.1500](https://doi.org/10.1038/nchembio.1500)
24. Pace NR (1997) A molecular view of microbial diversity and the biosphere. *Science* 276(5313):734–740
25. Altschul SF, Madden TL, Schaffer AA, Zhang J, Zhang Z, Miller W, Lipman DJ (1997) Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Res* 25(17):3389–3402
26. Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Höhna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP (2012) MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. *Syst Biol* 61(3):539–542. doi:[10.1093/sysbio/sys029](https://doi.org/10.1093/sysbio/sys029)
27. Huelsenbeck JP, Joyce P, Lakner C, Ronquist F (2008) Bayesian analysis of amino acid substitution models. *Philos Trans R Soc Lond B Biol Sci* 363(1512):3941–3953. doi:[10.1098/rstb.2008.0175](https://doi.org/10.1098/rstb.2008.0175)
28. Joshi NA, Fass JN (2011) Sickle: A sliding-window, adaptive, quality-based trimming tool for FastQ files (Version 1.33) [Software]. <https://github.com/najoshi/sickle>
29. Peng Y, Leung HC, Yiu SM, Chin FY (2012) IDBA-UD: a de novo assembler for single-cell and metagenomic sequencing data with highly uneven depth. *Bioinformatics* 28(11):1420–1428. doi:[10.1093/bioinformatics/bts174](https://doi.org/10.1093/bioinformatics/bts174)
30. Seemann T (2014) Prokka: rapid prokaryotic genome annotation. *Bioinformatics* 30(14):2068–2069. doi:[10.1093/bioinformatics/btu153](https://doi.org/10.1093/bioinformatics/btu153)
31. Beimgraben C, Gutekunst K, Opitz F, Appel J (2014) hypD as a Marker for [NiFe]-Hydrogenases in microbial communities of surface waters. *Appl Environ Microbiol* 80(12):3776–3782. doi:[10.1128/aem.00690-14](https://doi.org/10.1128/aem.00690-14)
32. Barz M, Beimgraben C, Staller T, Germer F, Opitz F, Marquardt C, Schwarz C, Gutekunst K, Vanselow KH, Schmitz R, LaRoche J, Schulz R, Appel J (2010) Distribution analysis of hydrogenases in surface waters of marine and freshwater environments. *PLoS ONE* 5(11):e13846. doi:[10.1371/journal.pone.0013846](https://doi.org/10.1371/journal.pone.0013846)
33. Levin DB, Pitt L, Love M (2004) Biohydrogen production: prospects and limitations to practical application. *Int J Hydrogen Energy* 29:173–185
34. Basak N, Das D (2007) The prospect of purple non-sulfur (PNS) photosynthetic bacteria for hydrogen production: the present state of the art. *World J Microbiol Biotechnol* 23:31–42
35. Kars G, Gunduz U (2010) Towards a super H<sub>2</sub> producer: improvements in photofermentative biohydrogen production by genetic manipulations. *Int J Hydrogen Energy* 35:6646–6656
36. Vanzin G, Yu J, Smolinski S, Tek V, Pennington G, Maness PC (2010) Characterization of genes responsible for the CO-linked hydrogen production pathway in *Rubrivivax gelatinosus*. *Appl Environ Microbiol* 76(11):3715–3722. doi:[10.1128/AEM.02753-09](https://doi.org/10.1128/AEM.02753-09)
37. Xing D, Zuo Y, Cheng S, Regan JM, Logan BE (2008) Electricity generation by *Rhodospseudomonas palustris* DX-1. *Environ Sci Technol* 42(11):4146–4151
38. Maness PC, Smolinski S, Dillon AC, Heben MJ, Weaver PF (2002) Characterization of the oxygen tolerance of a hydrogenase linked to a carbon monoxide oxidation pathway in *Rubrivivax gelatinosus*. *Appl Environ Microbiol* 68(6):2633–2636
39. Maness PC, Huang J, Smolinski S, Tek V, Vanzin G (2005) Energy generation from the CO oxidation-hydrogen production pathway in *Rubrivivax gelatinosus*. *Appl Environ Microbiol* 71(6):2870–2874. doi:[10.1128/AEM.71.6.2870-2874.2005](https://doi.org/10.1128/AEM.71.6.2870-2874.2005)
40. Ghirardi ML, Posewitz MC, Maness PC, Dubini A, Yu J, Seibert M (2007) Hydrogenases and hydrogen photoproduction in oxygenic photosynthetic organisms. *Annu Rev Plant Biol* 58:71–91. doi:[10.1146/annurev.arplant.58.032806.103848](https://doi.org/10.1146/annurev.arplant.58.032806.103848)
41. Parkin A, Bowman L, Roessler MM, Davies RA, Palmer T, Armstrong FA, Sargent F (2012) How *Salmonella* oxidises H<sub>2</sub> under aerobic conditions. *FEBS Lett* 586(5):536–544. doi:[10.1016/j.febslet.2011.07.044](https://doi.org/10.1016/j.febslet.2011.07.044)
42. Nishihara H, Miyashita Y, Aoyama K, Kodama T, Igarashi Y, Takamura Y (1997) Characterization of an extremely thermophilic and oxygen-stable membrane-bound hydrogenase from a marine hydrogen-oxidizing bacterium *Hydrogenovibrio marinus*. *Biochem Biophys Res Commun* 232(3):766–770. doi:[10.1006/bbrc.1997.6369](https://doi.org/10.1006/bbrc.1997.6369)
43. Nakatsu CH, Hristova K, Hanada S, Meng XY, Hanson JR, Scow KM, Kamagata Y (2006) *Methylibium petroleiphilum* gen. nov., sp. nov., a novel methyl tert-butyl ether-degrading methylotroph of the Betaproteobacteria. *Int J Syst Evol Microbiol* 56(Pt 5):983–989. doi:[10.1099/ijs.0.63524-0](https://doi.org/10.1099/ijs.0.63524-0)
44. Jeon CO, Park W, Ghiorse WC, Madsen EL (2004) *Polaromonas naphthalenivorans* sp. nov., a naphthalene-degrading bacterium from naphthalene-contaminated sediment. *Int J Syst Evol Microbiol* 54(Pt 1):93–97